

OM of: US-08-711-417C-165 to: A\_Geneseq\_032802: \* out\_format : pfs  
 Date: Aug 28, 2002 10:05 AM  
 About: Results were produced by the GenCore software, version 4.5.  
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Command line parameters:  
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 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPXT=0.000  
 -QGAPOP=4.500 -QGAPWT=0.050 -XGAPOPT=10.000 -XGAPWT=0.500  
 -FGAPOP=6.000 -FGAPWT=7.000 -YGAPOPT=10.000 -YGAPWT=0.500  
 -DELOP=6.000 -DELEXT=7.000 -SPART=1 -MATRIX=dlossum62  
 -TRANS=human40.cdi -LIST=45 -DOCALL=200 -THR\_SCORE=pct  
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 -USER=6228611\_qcgcnl\_1164 -NCPU=6 -ICPU=3 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPPXY -WAIT -THREADS=1

Search information block:

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 Query length: 1551  
 Database sequences: 747574  
 Database length: 111073796  
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AC AAW70971;	AC		
DT 11-JAN-1999 (first entry)	XX		
XX Human Ikaros isoform hik-1.	XX		
XX Ikaros; hik-1; transcription factor; human; lymphocyte; cell differentiation; T cell; cancer; immunodeficiency; Alzheimer's disease; therapy; diagnosis.	XX		
XX Homo sapiens.	OS		
XX	XX		
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:AAW72681 +	1005..00	1.514..24	1.4e-7
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Claim 1: Page 127-129; 15pp; English.

This is the amino acid sequence of human Ikaros protein isoform hik-1, deduced from a cDNA clone (see AA42840) obtained from a Jurkat T cell line cDNA library. Native Ikaros is active in the early stages of lymphocyte differentiation, binding to and activating the CD3-delta gene enhancer (see also AAW0964 and AAW70969) are isoforms that arise from differential splicing of Ikaros gene transcripts, and contain different combinations of zinc fingers. They are expressed primarily in T cells in the adult and may play a role as a genetic switch regulating entry into the T cell lineage. The human and murine sequences (see also AAW0963 and AAW70968) are very similar. The invention provides Ikaros nucleic acids, vectors and host cells expressing Ikaros polypeptides. These can be used to treat T and B cell diseases (e.g. immune deficiencies caused by

CC

drugs, radiation or cancer), to control expression of heterologous genes placed under control of an Ikaros element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplification or differentiation, especially in hematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences.

XX  
Sequence 516 AA;

alignment\_scores:  
 Quality: 2750.00 Length: 516  
 Ratio: 5.329 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-08-711-417C-165 x AAW70971 ..

Align seg 1/1 to: AAW70971 from: 1 to: 516

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 1 MetaspalaAspGluGlyLysPheSerGlyLysGlueSe 17

51 CCCCCCTGTAcCGATACTCCAGATGGGGATGAGCCATGCCATCC 100  
 51 ArgValAlaSerAsnValAspGluProLysPheSerGlyLysPhe 17

17 xProProvalSerAspHrProAspGluLysPheProLysPhe 34

101 CGAGGACCTCTCCACCCACTGGAGGACAGCAAGCTCAAGAGTGC 150  
 34 roGluAspLeuSerThrThrSerGlyGlnSerSerLysSerAsp 50

151 AGAGTCCTGGCAGTAATGCAAGTGGGGATGAGCCATGCCATCC 200  
 51 ArgValAlaSerAsnValAspGluProLysSerGlyLysAsp 67

201 TGGCGTGCCTCTGAATGAAATGAGTAAAGTAGAGACTCAAGTGATGAGAAGAA 250  
 67 nGlyA9GalactyGluMetAsnGlyLysGluLysSerGlyLysLeuArgM 84

251 TGGTTGATGCCCCTGGAGAGAAAATGAAATGCTCCACAGGGACCAAGGC 300  
 84 etLeuAspAlaSerGlyGluLysSerHisAspGlyGly 100

301 ACTCTGGCTTCTCTGGGACTCTGGCATTCTGACTCTAACGGAAACT 350  
 101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117

351 AAAGTGTGATACCTGTTGGATATTGTCATGGGCCAAATGTCATGG 400  
 134 aHisLysArgSerHisthGlyIleArgGlyLysSerGlyAsnGlnCys 150

401 TTCACAAAAGAGCCACACTGGAGAACGCCCCCTCCAGTCAGTGC 450  
 151 GlyAlaserPheThrGlnLysLysAsnLeuLeuArgHisthLysLeuHi 167

501 TGGGGGAGAGGCCCTCAAMTGCACACTGGCAACTACGCCGCGCC 550  
 167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyraCysArgA 184

551 GGAGGGACGCCCTCACAGGCCACCTGGGACCAACTCCGTTGTAACCT 600  
 184 rArgAspAlaLeuThrGlyHsIleArgGlyLysPro 200

601 CACAARANGTGGATATGTTGGCCGAACCTATAACAGCAGACTCTTAGA 650  
 201 HisLysCysGlyTyrCysGlyArgSerTyriySglArgThrSerLeuG1 217

651 GAAACATAAAAGCGCTGCCAACACTTGAAACCATGGCCCTTCGG 700

217 ||||||| GluHisLysGluArgCysHisAsnTyrlLeuGluSerMetGlyLeuProG 234

701 GCACACTGTTACCCAGCATTAAGAGAAACTAAAGCACAGTGGAAATGGCA 750  
 234 LysThrLeutyrProValIleLysGluLuthrLysSerGluMetAla 250

751 GAAGACCTGTCGAAGATAGGATGATCAGAGATCTCTGTTGGACAGACT 800  
 251 GluAspIeuCysLysSerGlySerGluArgSerLeuValLeuAspArgLe 267

801 AGCAAGTAAATGTCGCCRAAGCTAGAGCTCTATGCCCTCAGTGGAAATTCCTTG 850  
 267 uAlaSerAsnValAlaLysArgLysSerMetProGlnLysPheLeuG 284

851 GGGACAGGGCCCTGTCGACAGCCCTAAGCAGTGCCACCTACAGAAG 900  
 284 LysAspLysGlyLeuSerAspHrProTyraspSerAlaThrTyrglyLys 300

901 GAGAACGAAATCATGAAAGTCCACAGMGTGACCAAGCACAACAGC 950  
 301 GluAsnGluMetMetLysSerHisValMetAlaLeuAsnAla 317

951 CATCAACTACCTGGGGCGAGTCCCTGCGGCCGCTGGAGACGCC 1000  
 317 aIleAsnTyrlLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 334

1001 CGGGCCTTCCCAGGTTGGCTCATAGCCCGATGTTACAGCCGATGCGAC 1050  
 334 roGlyGlySerGluValProValIleSerProMetTyrlGlnLeuHis 350

1051 AGGGCCTCAGGGGGCACCCCGCGCTCCAACCAACTCGGCCAGGACAGGC 1100  
 351 ArgArgSerGluGlyHrProArgSerAsnHisSerAlaGinAspSerAl 367

1101 CGTGGAGTACCTGGCTCTGGCTCTGGCTCAGGCGAACCTGGAGGC 1150  
 367 aValGluTyrlLeuLeuUsertryAlaLysLeuValProSerGluA 384

1151 GCGAGGGTCCCAGGCAACGCTGGCTCTCCAAAGGCCAAGTGGCCCTCTGGAGC 1200  
 384 rgGluLysSerProSerAsnSerCysGlnAspSerThrAspThrGluSer 400

1201 AACAAAGGAGGAGGCCAGGGCTAGCTGCTCTTCTACCTGACAACCACATGC 1250  
 401 AsnAsnDluGluInArgSerGlyLeuLeuArgLeuThrAsnHistileA 417

1251 CCGACCGGGCAAACCGGTTGCTGCTCTCAAGGAGGACCGGCCCTAGCACC 1300  
 417 aArgArgGluInArgValSerLeuLysGluLysGluHisArgLysAlaTyAspL 434

1301 TGC TGCCGCCCTGGAGACTTCGGAGGAGCTCCAGGAGGCTGGCTGGTCAGC 1350  
 434 eLeuArgAlaAspSerGluAsnSerGlnAspAlaLeuArgValValSer 450

1351 ACCAGGGGGAGCAGATGAAAGTTGTAAGTGGCAACTTGCGAAACATGCCGGTCT 1400  
 451 ThreSerIleGluGluInMetLysValTyrlLeuLysGluLysArgValLe 467

1401 CTTCCTCNGATCACGTCATGTCACCATCACATGGGCTGCCACGGCTCC 1450  
 467 rGluAspProPheGluCysAsnMetCysLysTyrlHisSerGlnAspArgTyr 500

1501 GAGTTCTCCTCCACATAACGGGAGAACCTCCGTTCCACATGAGC 1548  
 501 GluPheserSerHistileHsIleArgGlyLysArgPhenylMetSer 516

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AC	AAB42333;	
DT	08-FEB-2001	(first entry)
DE	Human	ORFX ORF2097 polypeptide sequence SEQ ID NO:4194.
XX	KW	Human; open reading frame; ORFX; detection; cytostatic;
XX	KW	vulgaris; antipsoriatic; antiparkinsonian; nortropic; n
XX	KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressive
XX	KW	immunostimulant; thrombotic; coagulant; vasotropic; an
XX	KW	hypotensive; dermatological; immunosuppressive; antiinfl
XX	KW	antiviral; antibacterial; antifungal; antineumatic; ant
XX	KW	antihaemetic; gene therapy; cancer; proliferative disorder
XX	KW	neurodegenerative disorder; osteoarthritis; graft vs hos
XX	KW	cardiovascular disease; diabetes mellitus; hypothyroidis
XX	KW	cholesterol ester storage; systemic lupus erythematosus;
XX	KW	severe combined immunodeficiency; malaria; autoimmune di
XX	KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; bu
XX	KW	bone damage; cartilage damage; antiinflammatory disease;
XX	KW	thrombosis; contraceptive.
OS	XX	Homo sapiens .
PN	XX	WO2000058473-A2.
PD	XX	05-OCT-2000.
PP	XX	31-MAR-2000; 2000WO-US08621..
PR	XX	31-MAR-1999; 99US-0127607.
PR	XX	02-APR-1999; 99US-0127656.
PR	XX	05-APR-1999; 99US-0127728.
PR	XX	30-MAR-2000; 2000US-0540753.
PA	XX	(CURA-) CURAGEN CORP.
PI	XX	Shimkets RA, Leach M;
DR	XX	WPI; 2000-602362/57.
DR	XX	N-PSDB; AAC76542.
PT	XX	Novel nucleic acids and peptides derived from open reading frames useful for treating e.g. cancers, proliferative disorders neurodegenerative disorders and cardiovascular disease -
PT	XX	Claim 11: Page 3390-3391; 5507PP; English.
CC	CC	AAC74446 to AAC77606 encode the proteins given in AAB40233 which represent the human ORFX open reading frames 1 to 33 sequences have activities such as: cytostatic; hepatotrop
CC	CC	antipsoriatic; anticonvulsant; antiarthritic; coagulant; vasotropic; immunosuppressive; dermatological; immunosuppressive
CC	CC	antidiabetic; hypotensive; cardiotonic; antihypertensive; antineuritic; antifungal; antifungal; antifungal; antihyperthyroid; and antiaemic. The sequences can be used to treat pathological conditions associated with an ORFX-associated
CC	CC	nucleic acids can be used to express ORFX proteins in general vectors. The proteins and nucleic acids may be used to treat proliferative disorders, neurodegenerative disorders, osteo
CC	CC	graft vs host disease, cardiovascular disease, diabetes mell
CC	CC	erythematous, hypothyroidism, cholesterol ester storage, se
CC	CC	bacterial or fungal infection, malaria, autoimmune disorder
CC	CC	allergies, aplastic anaemia, burns, wounds, bone and carti
CC	CC	nocturnal haemoglobinuria, antiinflammatory disease; to en
CC	CC	coagulation; to inhibit thrombosis; and as a contraceptive.
Sequence	519 AA.	
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251	GluAspLeucysLysIleGlySerGluArgSerLeuValLeuAsparGle	267
801	ACCAACTAATTCGCCAAAGCTGATGGCTATGCCATGAAATTCTTGC	850
267	valSerAsnValAlaLysArgLysSerSerMetProGlnAllysPheLeuG	284
851	GGGACAGGGCTGTCCGACGCCCTAGAC...ATGCCAGCTAGAG	897
284	LysAsparGlyLeuAsparAspThrProTyAspSerSerAlaSerTyGlu	300
898	ARGAGAACGAAATGTAAGTCCACCGTGATGGACCAAGCATCAACAA	947
301	LysGluLysGluMetIleSerHisValMetSpGlnAlaIleAsnAs	317
948	CGGATCACTACTCTGGGGCGGAGCTCCNGGCCGCTGGTCCAGAGC	997
334	ropGlyGlySerGluValProValProMettyGlnLeu	350
1048	CACAGG...CGCCTGGAGGGCACCCCGCTCAACACTCGGCCAGGA	1093
351	HistysProLeuAlaGlyIleGlySerArgSerAsnHistSerAlaGlnAs	367
1095	CAGGCCGCTGGGAACTTCTGCTGCTCTCCAAAGCCAAGTTGTGCCCC	1144
367	serAlaValGluAsnLeuLeuLeuUserLysAlaLysLeuValPro	384
1145	CGAGCGGCGAGGGTCCCGAGAACAGCTCCAGGGACACC	1171
384	ergLysArgGluIaLaserProSeAsnSerCysGlnAspSerThrasPthr	400
1195	GAGAGAACACAGCAGGAGAACAGCTGCCAAAGACTCCAGGGACACC	1241
401	GluserAsnAsnGluGluGlnArgSerGlyLeuIleIleLeuThrAsnH	411
1245	CATGCCGCGAGGCCAAC...GTGTCGCTCAAGGAGGAGCACCGCG	1251
417	sileAlaProHisAlaArgAsnGlyLeuSerIeUlysGluGluHisArg	43
1292	CCTAGGACCTGCTGGCCGCCCTCGGAACCTGCGAACGCGCTCCGC	13
434	IleTyrasPLeuValArgAlaIaSerGluAsnSerGlnAspAlaLeuHarg	45
1342	GTCGGTCAAGCACCAGGGGACAGATGAAAGCTGATCAAGTGGCAACACTG	13
451	ValValSerThrSerGlyGluInMetLysValIleIleLysCysGluHisC	46
1392	CGGGGTGCTCTGGATCACGCTCATGTCACCCATCCACATGGCTGCC	14
467	sAGValLeuPheLeuAspHisValMetTyrrhileHisMeIgLyCysH	48
1542	CATGAGC	154
517	sMetsTer	519
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seg documentation\_block;

AAR46964

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 1288 CGGCCATCAGACTCGTGCAGCGCCGCTCCGACAACACTCGCAGCGCCT 1337  
 449 ArgAlaIyraspIeuAlaArgAlaAsnSerGlnAsnSerGlnAspAlaph 465  
 1338 CGCGTGTCTAGCACCGGGAGGAGATGAGGGTGTACAAAGTGGAAC 1387  
 465 eargvalValSerThrSerGlyLysGluGinMetLysValTyrLysCysGluH 482  
 1388 ACTGCCGGTGTCTGTCTGTGATCACCTCATTGACACATGGC 1437  
 482 lscysArgValLeuPheLeuAspHisValMetTyrThrIleHisMetGly 498  
 1438 TGCCACGGCTTCGATCGTGAATCCATTGAGTCACATGCGCTTACACAG 1487  
 499 CyshisGlyPheArgaspProPheGluCysthrMetCysGlyTyrisse 515  
 1488 CCAGGACGGTAGCAGATTCTGTGCCACATAACGCCAGGGAGCACCGCT 1537  
 515 rglnAspArgTyrGluPheSerSerHisIleThrArgGlyLysLysArg 532  
 1538 TCCACATGAGC 1548  
 532 heHisMetThr 535

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XX	
DT	09-MAY-1996 (first entry)
XX	
DE	Human Ikarus protein hIk-1.
XX	
KW	Ikarus; transgene; transgenic animal; transgenic mouse; hIk-1;
KW	immunocompromised; immune system disorder; nervous system disorder;
KW	animal model.
XX	
OS	Homo sapiens.
XX	
PN	WO9604372-A1.
XX	
PD	15-FEB-1996.
XX	
PF	28-JUL-1995; 95WO-US09345.
XX	
PR	29-JUL-1994; 94US-028330.
XX	
PA	(GEHO ) GEN HOSPITAL CORP.
PI	Georgopoulos K;
XX	
DR	WPI: 1996-129389/13.
DR	N-PSDB; AAR16066.
PT	
PT	Transgenic rodent having Ikarus trans-gene (pref. mutated) - is
PT	severely immuno-compromised and can be used as model to determine
PT	effects of treatment for immune and nervous system disorders
XX	
DISCLOSURE:	Fig 2; 102pp; English.
XX	
CC	An almost full-length cDNA sequence (AA196060) codes for part
CC	(AAR92015) of the human Ikarus protein, a zinc finger protein that
CC	a master regulator of haematopoietic differentiation and a major
CC	determinant in lymphocyte specific differentiation and development. Different
CC	isotforms (see AAR92014 and AAR92016-19) of mouse Ikarus have also been isolated. Transgenic animals, pref. mice, having a mutated Ikarus
CC	transgene, esp. a mutation in the zinc finger domain, have also been isolated.

CC Ikaros protein, are used as models to determine the effects of CC treatments for immune or nervous system disorders.

XX Sequence 461 AA;

alignment\_scores:  
 Quality: 2467.00 Length: 461  
 Ratio: 5.351 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000  
 alignment\_block:  
 US-08-711-417C-165 x AAR92015 ..

Align seg 1/1 to: AAR92015 from: 1 to: 461

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216	AATAATGGGAGAAATGTGCCAGGATTAGCAAGTGCTGTGCTGTGCG	265	...     ...     ...     ...     ...     ...     ...     ... 17 umetAsnGlyLysGluCysAlaGluAspLeuArgMetLeuAspAlaSerG
266	GAGACAAATGAAATGGCICCCACAGGGACCAGGCACCTGGCTTGTCG	315	...     ...     ...     ...     ...     ...     ... 34 LysGluLysMetArgGlySerHisArgAspGlnLysSerAlaLeuSer
316	GGAGTTGGAGGCAATCGACTTCTTAACGAAAAACTAAAGTGATATCTG	365	...     ...     ...     ...     ...     ... 67 sGlyLysIleCysIleGlyProAsnValLeuMetValHisLysArgSerH
366	TGGGATCATTTGCAATCGCAGTCTCTAAGCTTCTAGCTGTCACAAAAGAGCC	415	...     ...     ...     ...     ... 51 GlyvalGlyLysIleArgLeuProAsnGlyLysLeuLysCysAspIleC
416	ACACTGGAGACGGCCCTTCAGTCAATCGTGCCTGCGGCCATTCACC	465	...     ...     ...     ... 84 15thArgLysGlnArgProPheGlnCysAspGlnCysGlyAlaSerPheHr
466	CAGAAGGGCACCTGCTGTCGGCACATCGCTGAGAAGGCC	515	...     ...     ... 101 GluLysGlyAlaLeuLeuGlnLeuGlnLeuGlnSerGlyLysSpr
516	CCTCAAATGCCACCTCTGCAACTAGGCCCTTCGCGGAGGCCCTCA	565	...     ... 117 oPhelLysCysHisLeuCysAsnTyAlaCysTargAspAlaLeut
566	CTGGCCACCTGAGGAGGCACCTCGGTGCTAAACCTCACAATGTGGATF	615	...     ... 134 hrGlyHisLeuArgThrHisSerGlyLysSphoHisLysGluLys
616	TGTGGCCAAAGCTATAAACCGCAACTGGCTCTTAGGAAACATAAGAGCG	665	...     ... 151 CysGlyArgSerTerIleLysGlySerArgThrSerIeuGluLysGluLys
666	CTGGCACACACTTGGAAAGCATGGCCCTCCGGGCACACTSPACCCAG	715	...     ... 167 9GlyHisAsnTyLeuGluSerMetGlyLeuProGlyThrLeuTyPr
716	TCATTAAGAGAAACTAACGCAAGTGTGAATGGCAGAAGACCTGTGCAAG	765	...     ... 184 alleleLysGluGluThrLysHisSerGluMetAlaLysAspLysCysLys
766	ATAGGATCAGAGAGATCTCTGCTGAGACTGCAAGTAAATGTCG	815	...     ... 201 IleGlySerGluLysSerLeuValLeuAspArgLeuSerAsnValAl
816	CAAACGTAAAGAGCTCTATGCCCTCAGAAATTTCTGGGACAAAGGCCGT	865	...     ... 217 aLysArgLysSerSerMetProGlnLysPhalLeuGlyAspLysGlyLeu
866	CCGACACGCCCTACGACAGTGGCACGTACGGAGAAGGAAATGATG	915	...     ... 234 erAspThrProTyraspSerAlaThrTyrgLysGluAsnGluMetMet
916	AAGTCCCACCTGATGCAAGGCTATCACAAAGCCATCAACTACCTGGG	965	...     ... 251 LysSerHisValMetAspGlnAlaLeuAsnAsnAlaLeuAsnTerLeuGly
966	GGCCGAGTCCCTGGCCCCGGCTGGAGAGCCCCCGGGTTCCSAGG	1015	...     ... 267 YALAGLuseRLeuAGProLeuValGlnThrProProGlySerGluV
1016	TGGTCCGGCATCATGCCGATGTACCCAGTGGCACACGGCAGCAGGGC	1065	...     ... 284 alaValProValLeSerProMetYrgLysGluLeuHisArgArgSerGluGly
1066	ACCCCGGCTCCAAACACTGGCCAGGAAGAGCCGCTGAGTACCCCTGCT	1115	...     ... 301 ThrProArgSerAsnHisSerAlaValGlyLeuLeuValGlyLeuLeu
1116	GCTGCTCTCAAGGCAAGTGTGGCTGCCCTGGAGGCGAGGCCTCCCGGA	1165	...     ... 317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerLeuPro
1166	GCACAGCTGCCAAGACTCCAGGACACCAGAGCAACACGAGGAGCAG	1215	...     ... 334 erAsnSerCysGlnAspSerThrAspThrGluSerAsnGluGluGln
1216	CGAGGCGCTCTATCPACTGACCACCATGCCGCACTGCCTGGCGCAAC	1265	...     ... 351 ArgSerGlyLeuLysTerLeuThrAsnHisTerLeuArgArgAlaGlnAr
1266	CGGCTGCTCAAGGAGGACCGCCGCTAGACCTGCTGGCGCGCT	1315	...     ... 367 gValSerIeuLysGluLysIleGlySerGlyLysArgAlaAlaLys
1316	CCGAGAACTCGAGGAGGCGCTCGGCTGCTGGCAGCACCGGGAGCAG	1365	...     ... 384 ergLysAsnSerGlnAspAlaLysLeuValSerThrSerGlyLeuGln
1366	ATGAGGCTACAGTGGAAACTGCGCTCTCTCTGATCACGT	1415	...     ... 401 MetLysValTyryLysCysGluLysCysArgValLeuPheLeuAspHisVa
1416	CATGTAACCATCCACATGGCTGCCGCTTCGGTGAATCCTTTGAGT	1465	...     ... 417 1MeTyrThrIleIleMetGlyCysHisLysPheArgAspProPheGluC
1466	GCAACATGCGGCTACACAGCGGACCCGTTCTCGTGGCAC	1515	...     ... 434 ysAsnMetCysGlyLysTerSerGlnAspArgTygGluPheSerSerHis
1516	ATAACGCGACGGGACACCCGCTTCACATGAGC	1548	...     ... 451 IleThrArgGlyGluHisArgPheHisMetSer

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseqp.embl/AA1998.DAT : AAW72672  
 seq\_documentation\_block:

ID	AAW72672 standard; Protein: 461 AA.
XX	
AC	AAW72672;
XX	
DT	14-JAN-1999 ( first entry)
XX	
DE	Human Ikaros.
XX	
KW	CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
KW	differentiation marker; immune system; corpus striatum; AIDS;
KW	Alzheimer's disease.
XX	
OS	Homo sapiens.
XX	
PN	US5824770-A.

XX 20-OCT-1998.  
 XX PD  
 XX 05-JUN-1995; 95US-0465590.  
 XX PF  
 PR 02-MAY-1994;  
 PR 94US-0238212.  
 PR 14-SEP-1992;  
 PR 92US-0946233.  
 PR 14-SEP-1993;  
 PR 93US-0121438.  
 PR 05-JUN-1995;  
 XX 95US-0465590.  
 XX PA (GEHO ) GEN HOSPITAL CORP.  
 XX PI  
 XX Georgopoulos K;  
 XX DR WPI-1998-582621/49.  
 DR N-PSDB; AAV65969.  
 XX PT  
 PT Ikarios poly-peptide(s) - useful for treating disorders of immune system or corpus striatum  
 XX PS  
 PS Claim 1; Column 55-58; 111pp; English.  
 XX  
 CC The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFkB element or an Ikarios binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFkB element or an Ikarios binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikarios isoform to any of a delta A element, an NFkB element or an Ikarios binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikarios binding to Ikarios responsive elements; or (e) it inhibits protein/protein interactions of transcriptional complexes formed with naturally occurring Ikarios isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFkB elements and/or Ikarios binding oligonucleotides, bind to delta A elements, NFkB elements and/or Ikarios binding oligonucleotides to competitively inhibit binding of naturally occurring Ikarios isoforms to delta A elements, NFkB elements and/or Ikarios binding oligonucleotides, competitively inhibit Ikarios binding to Ikarios responsive elements and/or inhibit protein/protein interactions of transcriptional complexes with naturally occurring Ikarios isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence represents a specifically claimed human Ikarios protein.  
 XX Sequence 461 AA:  
 alignment\_scores:  
 Quality: 2467.00  
 Ratio: 5.351  
 Percent Similarity: 100.000  
 alignment\_block:  
 US-08-711-417C-165 x AAW72672 ..  
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 1 AsnValAsnValGluThrGlnSerAspGluAsnGlyArgAlaCysG1 17  
 216 ATGAAATGGGAGAACGACTGAGCTGAGTGGAAAGCAGAAGGGCTGGTGA 215  
 17 uMetAsnGlyGluGluAspLeuArgMetLeuAspAlaSerG 34  
 266 GAGAAATGGGAGAACGACTGAGCTGAGTGGAAAGCAGAAGGGCTGGTGA 315  
 34 lGluIuLysMetAsnGlySerHisArgGlnGlySerSerAlaLeuSer 50  
 316 GGAGTGGGAGGCATCGACTTCCTAACGAAAACAACTAATGCTGATATCG 365  
 51 GlyValGlyGlyIleArgLeuProAsnGlyLeuLysCysAspIlecy 67

1266 CGTGTGCGCTCAGGGAGCACGGCCCTACGACCTGCTGGCCGCCGCCT 1315  
 367 gvalserleulysGluGluHsArgAlaIys 384  
 1316 CGAGAACTCGAGGACGCGTCAGCACCAGGGAGCAG 1365  
 384 ergluAsnSerGlnAspAlaLeuArgValSerThrSerGlyGluGln 400  
 1366 ATGAAGGGTAGCAAGTGGAAACTCCGGGTCCTGGATCACCT 1415  
 401 MetIysValTrpIlysCysGluIlysArgValLeuPhelleuAspHisVa 417  
 1416 CATACACCATCACATGGCTCACGGTTCCGTGAGCTTGAGT 1465  
 417 1-MethylTrpIleHisMetGlyCysIshGlyPheArgAspProheGluC 434  
 1466 GCAACATGTCGGTACACAGCGCAGSACCGGTACAGTCTCGTGCAC 1515  
 434 yasnMetCysGlyTyrrHisSerGlnaspArgTyrHisSerSerHis 450  
 1516 ATAAGCGGAGGGAGCACCGTCCACATGAC 1548  
 451 IleThrArgGlyGluHsArgPheHisMetSer 461

seq\_name: /SIDS1/gcqdata/hold-genesed/geneseq-p-emb1/AA1998.DAT:AAW70964

seq\_documentation.block:  
 ID AAW70964 standard; Protein; 461 AA.

XX AAW70964;

AC XX

DR DT

11-JAN-1999 (first entry)

XX DE Human Ikarus isoform hik-1.

XX KW Ikarus; hik-1; transcription factor; human; lymphocyte; cell differentiation; T cell; cancer; immunodeficiency; Alzheimer's disease; therapy; diagnosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 64..84 /note= "zinc finger motif"

FT Region 92..112 /note= "zinc finger motif"

FT Region 120..140 /note= "zinc finger motif"

FT Region 148..169 /note= "zinc finger motif"

FT Region 406..426 /note= "zinc finger motif"

FT Region 434..456 /note= "zinc finger motif"

FT Region 457..461 /note= "zinc finger motif"

XX PN CR2194256-A.

XX PD 05-MAR-1998.

XX PF 02-JAN-1997; 97CA-2194256.

XX PR 05-SEP-1996; 96US-0711417.

XX XX (GBIO ) GEN HOSPITAL CORP.

XX PI Georgopoulos K;

XX PR 1998-378292/33.

DR N-PDB; AAV42806.

XX PT New nucleic acid encoding Ikarus protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and

PT to control cell differentiation

XX Claim 7; Page 70-72; 158pp; English.

PS This is the amino acid sequence of human Ikarus protein isoform hik-1, deduced from a cDNA clone (see AAV42806) obtained from a CC Jurkat T cell line cDNA library. Native Ikarus is active in the CC early stages of lymphocyte differentiation, binding to and activating the CD3 delta gene enhancer (see AAV42804). Proteins CC of the human Ikarus family (see also AAW70969 and AAW70971) are CC isoforms that arise from differential splicing of Ikarus gene CC transcripts, and contain different combinations of zinc fingers. CC They are expressed primarily in T cells in the adult and may play a CC role as a genetic switch regulating entry into the T cell lineage. CC The human and murine sequences (see also AAW70963 and AAW70965-68) are CC very similar. The invention provides Ikarus nucleic acids, vectors CC and host cells expressing Ikarus Polypeptides. These can be used CC to treat T and B cell diseases (e.g. immune deficiencies caused by CC drugs, radiation or cancer), to control expression of heterologous CC genes placed under control of an Ikarus-responsive element, to CC treat nervous system diseases (e.g. Alzheimer's disease) and to CC modulate cell division, amplification or differentiation, especially CC in haematopoietic cells. Some Ikarus isoforms are antagonistic of CC others and may be used to inhibit interaction with DNA sequences. CC

SQ Sequence 461 AA;

alignment\_scores:  
 ID AAW70964 from: 1 to: 461

XX Align seg 1/1 to: AAW70964 from: 1 to: 461  
 1 AsnIvalLyvalGluIutGlnSerAspGluIuashGlyArgAlaCysG1 17

166 ATGTTAAAGTAGAGTCACTAGTGTAAAGAATGCGCTGCTGTA 215

166 ATGTTAAAGTAGAGTCACTAGTGTAAAGAATGCGCTGCTGTA 215

166 ATGATGGAAAGAACATTGCGGAGGATTACGAAATGCTGTATGCCCTGG 265

216 ATGATGGAAAGAACATTGCGGAGG

616 TGTGGCGAAGCTATAACAGGAAACGTCAGCTTATAGGAAACATAAAGACG 665  
 151 CysGlyArgSerTyLySgInArthrSerLeuGluLysGluIgln 167  
 666 CTGCCACAACACTTGAAAGCAAGGCCCTTCGGCACACCTAACCCAG 715  
 167 qCysHisAsnTyLeuGluSerMetGlyLeuProGlyThrLeuTyProl 184  
 716 TCAATRAAGAGAACTAACGACAGTGAATGCGAAGAACGCTGCGAAG 765  
 184 aLysLysGluLysGluLysHisserGluMetAlaGluAspLeuCysLys 200  
 766 ATAGGATCAGAGAGATCTCGTGTGGACAGACTAGCAAGTAATGTCGC 815  
 201 IleGlySerGluArgSerLeuValLeuPArgLeuAlaSerIvaAl 217  
 816 CAAACGTAAGAGCTCATGGCTCAGAAATTCTCTGGGACAAGGGCCTCT 865  
 217 aLysArgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeuA 234  
 866 CGACACGCGCTTAAGACAGTGCAAGTAGAGGAGAACGAAATGATGATG 915  
 234 1aAspThrProTyRaspSerAlaThrTyRgluLysGluIvaGluMetMet 250  
 916 AGTCCCOACGTGATGCCAACAGCCATCACAGCCATCAACTACCTCTGG 965  
 251 LysSerHisValMetAspGlnAlaLysAlaLysAsnAlaLysAsnAlaLys 267  
 966 GCGCGAActCCCTGCGCCGCTGGTGGAGACGCCCGGGGTTCCGAGG 1015  
 267 yAlaGluAlaLeuArgProLeuValGlnThrProProGlyGlySerGluV 284  
 1016 TGTTCGGCCTCATCACGCCATGTCAGATGCAAGGGCTCGAGGGCC 1065  
 284 aValProValLeuSerProHettyleyGlnLeuHiSArgArgSerGluGly 300  
 1066 ACCCGGGCtccAAACCCTGGCCCAGAGGCCGCTGGAGTACCTGCT 1115  
 301 ThrProArgSerAsnHisSerAlaLysGluAspSerAlaValGluTyLeuL 317  
 1116 GCTGCTCTCAAGGCCAAGTGTGCCCTCGAGGGCAGGGCtcccGA 1165  
 317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerPro 334  
 1166 GCAACAGCTGCCAAGACTCCAGGACCCGAGAACACGAGGAGGAGCAG 1215  
 334 eAsnSerCysLysInAspSerThrAspThrGluSerAsnAsnGluGluGln 350  
 1216 CGAGCGGTCTPATCPATCAGCAACCACATGCCCGAGGGCtccGAACG 1265  
 351 ArgSerGlyLeuLileyLeuThrAsnHisIleAlaArgGalaGlnAr 367  
 1266 CGTGTGCTCAGGAGGACCCGACCCGCTTACGACCTGCTGCCGCCGCT 1315  
 367 gValSerLeuLysGluGluHisArgAlaLysAspLeuSerGluGluAlaAlas 384  
 1316 CGGAGAACCTGGTAACTGGAAACACTGGCGGCTTCCtGATCACGT 1415  
 384 erGluAsnSerGlnAspAlaLeuArgAlaValSerThrSerGluGluGln 400  
 1366 ATGAAAGGTGTAAGTGGAAACACTGGCGGCTTCCtGATCACGT 1415  
 401 MethylsValTyryLysCysLysIvysSargAlaLeuPhelLeuAspIvsVa 417  
 1416 CANGTACACCATTCCACATGGGGTGGCAGGGCtCCGtGATCCTTtGAGT 1465  
 417 1MetylThrLileHisMetGlyCysHisGlyIglnAspProPheGluC 434  
 1466 GCAACATGCGCTTACACAGGAGACCCGTTACAGATTCGtGCGtGAC 1515  
 434 YsAsnMetCysGlyTyHisserGlnAspArgTyGluPheSerSerHis 450

1516 ATAACGGCAGGGGAGGACCCGCTTCCACATGAGC 1548  
 451 IleThrArgGlyGluLysArgPhethisMetSer 461  
 seq\_name : /SIPS1/gcgdata/hold-geneseq/geneseq-p-embl/AA1996.DAT.AAR92017  
 seq\_documentation\_block:  
 ID AAR92017 standard; Protein; 518 AA.  
 XX  
 AC AAR92017;  
 XX  
 DT 09-MAY-1996 (first entry)  
 XX  
 DE Murine Ikaros protein MIK-1.  
 XX  
 KW Ikaros; transgene; transgenic animal; lymphocyte;  
 KW immunocomprised; immune system disorder; nervous system disorder;  
 KW animal model; MIK-1.  
 XX  
 OS Mus musculus.  
 XX  
 Location/Qualifiers  
 FH Key 119..140  
 FT Domain /label= F1  
 /note= "zinc finger domain F1"  
 147..167  
 FT Domain /label= F2  
 /note= "zinc finger domain F2"  
 175..195  
 FT Domain /label= F3  
 /note= "zinc finger domain F3"  
 203..224  
 FT Domain /label= F4  
 /note= "zinc finger domain F4"  
 460..480  
 FT Domain /label= F5  
 /note= "zinc finger domain F5"  
 491..513  
 FT Domain /label= F6  
 /note= "zinc finger domain F6"  
 XX  
 WO9604372-A1.  
 PN  
 XX  
 PD 15-FEB-1996.  
 XX  
 28-JUL-1995; 9510-050345.  
 XX  
 PR 29-JUL-1994; 94US-0283300.  
 XX  
 (GEHO ) GEN HOSPITAL CORP.  
 XX  
 Georgopoulos K;  
 XX  
 WPI: 1996-129389/13.  
 DR N-PSDB; T01662.  
 XX  
 Transgenic rodent having Ikaros trans-gene (pref. mutated) - is  
 PT severely immuno-compromised and can be used as model to determine  
 PT effects of treatment for immune and nervous system disorders  
 XX  
 Disclosure; Fig 4; 102pp; English.  
 XX  
 CC The sequence of 57.5 kDa mouse Ikaros protein MIK-1 (AAR92017) was  
 CC deduced from mouse Ikaros cDNA (AA115062) isolated from a mature  
 CC T-cell line E15 library. Ikaros Protein is a master regulator of  
 CC hemopoietic differentiation and a major determinant in lymphocyte  
 CC differentiation. Other isoforms of Ikaros (see AAR92014, AAR92016 and  
 CC AAR92018-19) arise from differential splicing of Ikaros gene  
 CC transcripts. Transgenic animals, esp. mice, having a mutated Ikaros  
 CC transgene, esp. a mutation that alters the DNA binding domain of the  
 CC Ikaros protein, are used as models to determine the effects of  
 CC treatments for immune or nervous system disorders.  
 XX

Q	Sequence	518 AA;
	alignment_scores;	
	Quality: 2437.00	Length: 521
	Ratio: 4.913	Gaps: 6
	Percent Similarity: 95.202	Percent Identity: 89.635
	Alignment_block:	JGS-08-711-417C-165 x AAR92017 ..
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1	MetAspValAspLysGlyLysAspMetSerGlnValSerGlyLysGluSe 17	
51	CCCCCCCTGTTAAGGGATACTCCAGATGAGGGCATGCCATGCCATCC 100	
17	rProValSerAspThrProaspProGlyLysGluProMetProValP 34	
101	CCGAGGACACTCTCACCCACCTCGGGAGAACAGCAAAAGCTCCAGAGTGAC 150	
34	roGluAspLysSerThrSerGlyAlaGlnGlnAsnSerIysSerAsp 50	
151	AGAGTCGGCCAGTAATGTTAAAGTAGACTCAGAGTGATGAAAGGAA 200	
51	ArgGlyMetAlaSerAnVallysValGluThrGluSerAspGluGluas 67	
201	TGGGGTGTGCTCTGTGAAATGGAATGTTGGGAGGATTACGAA 250	
67	nGlyArgLysGluLysSerGlyLysGluLysAlaGluAspLeuArgM 84	
251	TGCTTGTATGCCCMGGGAGAGAAAATGAATGGCTCCACAGGACCAGGC 300	
84	etLeuAspAlaSerGlyAlaGlyLysMetAsnGlySerIysAspGlnGly 100	
301	AACTCGGGCTTGTGGAGTTGGGGATGAGCTTGACTACGGAAACT 350	
101	SerSerAlaLeuSerGlyAlaGlyLysLeuProAsnGlyLysLe 117	
351	AAAGTGTGATACTGTCGATCATTCGATCGGGCCCAAUATGCTCATGG 400	
117	uLysCysAspLysLeuValCysLeuValCysLeuMet 134	
401	TTCACAAAAGAGCCACACTGGAGAACGGCCCTTCCAGTCAATCAGTGC 450	
134	AlaHisLysArgSerHisthrgLysGluArgProProGlyCysAsnSer 150	
451	TTCGGGGAGAGGCCCTCAAATGCCAACACTAGGCCACTCTGCC 500	
151	GlyAlaSerProThrGlyLysGlyAsnLeuLeuArgHisIleLeuH 167	
501	TTCGGGGAGAGGCCCTCAAATGCCAACACTAGGCCACTCTGCC 550	
167	sSerGlyLysProPhyLysCysHisLeuCysAsnTyrAlaCysArgA 184	
551	GGAGGGACGCCCTCACTGGCCACCTTGGAGGAGCCACTCGTGGTAACCT 600	
184	rGargAspAlaLeuThrGlyLysLeuArgThrHisSerValGlyLysPro 200	
601	CACAAATGTGSAATATTGGCCGAAGCTATAAACAGGAACTAGCACAGTGAATGGCA 750	
201	HisLysCysGlyTytCysGlyArgSerTyrFlysGlnArserSerLeuG 217	
651	GGAAACATAAAGAGCCGCTGCCACAACACTACTGGAAAGCAGGGCCCTTCGG 700	
217	uGluHsLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuPrG 234	
701	GCACACTGTACCCAGTCATAAAGAGAACTAGCACAGTGAATGGCA 750	
234	IY..ValCysProValIleLeuGluGluThrAsnHisAsnGluMetAla 249	
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	ID AW7267 standard:	Protein: 518 AA.
	514 qTyHisIleuSer 518	

AAW72674; 14 -JAN-1999 (first entry)

Mouse Ikaros mik-1.

CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease.

Mus sp.

US5824770-A.

20-OCT-1998. 05-JUN-1995; 95US-0465590.

02-MAY-1994; 94US-0238312. 14-SEP-1992; 92US-0946233. 14-SEP-1993; 93US-0121438. 05-JUN-1995; 95US-0465590.

(GEHO ) GEN HOSPITAL CORP.

Georgopoulos K;

WPI; 1998 582621/49.  
N-PDB; AAV6691.

Ikaros poly:peptide(s) - useful for treating disorders of immune system or corpus striatum

Claim 1; Column 61-66; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides competitively inhibit Ikaros binding to Ikaros responsive elements and inhibit protein-protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence represents a specifically claimed mouse Ikaros protein.

Sequence 518 AA;

segment\_scores:  
Quality: 2437.00 Length: 521  
Ratio: 4.913 Gaps: 6  
Percent Similarity: 95.202 Percent Identity: 89.635

segment\_block:  
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sign seg 1/1 to: AAW72674 from: 1 to: 518

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951 CATCAACTACCTGGGGCCGAGTCCTGCCGTGGTCAAGAGCCCC 1000  
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 315 alleASTYrLeuGylAlaGluSerLeuArgProIleuValThrProP 332  
 1001 CGGGCGTTCCGAGGTTGTCGGCATCACCCGATGTACCGTGCAC 1050  
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 332 rodySerSerLeuValIvaProIleSerSerMetYrgLLeuHis 348  
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 1058 CGCGTGGAGTACCTGGCTCTCGTCCTCAGGCCAAGTTGGGCCCTCGG 1147  
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 1248 CGCCCGAGGCCAACGC...GTCGCTCAAGGAGGACCCGGCCCT 1294  
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 414 eAsnProHisAlaArgAsnGlyLeuAlaLeuIleTerLeuIleAsnHisI 431  
 1295 AGCGACTGTGCGGCCGCTCGAGACTCCAGGACGGCTCCCGCTG 1344  
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 1345 GTCAAGCACCAGGGAGGAGGAGTAAGTGTGACACTGGCCG 1394  
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 448 ValSerThrSerGlyGluGlnLeuLysValThrLysGluHisCysAsR 464  
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 1436 GCTGCCACGSGCTTCGGTAGTCATGCAACATGTGGGCTTACAC 1485  
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 1486 AGCCAGGACCGTAGAGTTCTGAGTCACATGCGGCTTACAC 1535  
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 AC AAW70966;  
 XX DT 11-JAN-1999 (first entry)  
 XX DE Mouse Ikarus isoform mlk-1.  
 XX  
 KW Ikarus; mlk-1; transcription factor; mouse; lymphocyte;  
 KW cell differentiation; T cell; cancer; immunodeficiency;  
 KW Alzheimer's disease; therapy; diagnosis.  
 OS Mus sp.  
 XX FH Key Location/Qualifiers  
 FT Region 119..139 /note= "zinc finger motif"  
 alignment\_scores:  
 ID AAW70966 from: 1 to: 518  
 Length: 521  
 Gaps: 6  
 Percent Identity: 89.635  
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 US-08-711-417C-165 x AAW70966 ..  
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 1 ATGGATGCTGAGGAGTCAGATGCTTCATGGGAAGGAAG 50  
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 1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17  
 51 CCCOCCTSTAAGGATACTCCAGATGAGGGCATGCCCATGCCATGCCATGCC 100  
 ||||:|||:  
 .

Region	Qualifiers
1..53	/label= Exons 1/2.
Region	54..141
	/label= Exon 3.
Region	142..247
	/label= Exon 4.
Region	248..288
Mus musculus.	
AAR46565;	
21-Oct-1994 (first entry)	
Ikaros zinc finger protein isoform IK-1.	
Ikaros; zinc finger; protein; immune disorder; therapy; tree	
corpus striatum; regulatory gene.	
q_name: /SIDSI/gcadata/hold-generated/geneseqp-emb1/AA1994.DAT:A	
q_documentation_block:	
AAR46565 standard; Protein: 568 AA.	

Alignment scores:  
Quality: 2422.00 Length: 571  
Ratio: 4.863 Gaps: 7  
Percent Similarity: 87.215 Percent Identity: 82.137

alignment\_block:  
US-08-711-417C-165 x AAR46965 ..

Align seg 1/1 to: AAR46965 from: 1 to: 568

51 CCCCCCTGTAAAGCGATACTCCAGATGAGGGCGATGAGGCCATGCCGAICC 100

17 rProProValSerAspThrProAspGluGlyAspGluProMetProAlaP 34

51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGuaas 67

201	TGGGGCTGCGCTGTGAATGAACTGGGGAAAGAATGTCGGGAGGATTACGAA	250
67	DGLYVPROALACVSGLIMETASNGLVCIGLICUSVSLASLQVQVAVV	94

84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100

300 ..... 300  
101 SerSerialUserSerialWallClock ..... 117

300 ..... 300

117	uLyscysAspIleCysGlyIleValcysIleGlyProAsnValLeuMetV	134
300	.......	300
134	alHsLysArgSerHisthrGlyGluArgProHeGlnCysAsnGlnCys	150
301	AGCTGGCTTGTGGACTTGGCATTCGACTTCCTAACGGAAAACCT	350
151	:     :     :     :     :     :     :     : SerSerAlaLeuSerGlyValGlyValGlyTleArgLeuProAsnGlyLysLe	167
351	AAACTGTGTATATCTGGATCATTTCATCGGGCCCAATGTGCATGG	400
167	uLyscysAspIleCysGlyIleValcysIleGlyProAsnValLeuMetV	184
401	TTCACAAAGAACCCACACTGGAAACGGCCCTCCGGCACATCAAGCTGC	450
184	alHsLysArgSerHisthrGlyGluArgProHeGlnCysAsnGlnCys	200
451	GGGCCCTATTCACCCAAAGGCCAACCTGTGCACCTAGGCCCTGCCGCC	550
217	ssGlyGlyLysProPhelysCysHisLeuCysAsnTyRArgcysArgA	234
551	GGAGGGAGGCCCTCATGGCCACACTGGACGACCTCGTGGTAACCT	600
234	rgargAspAlaLeuThrGlyHisLeuLeuArgThrHisSerValGlyLysPro	250
601	CACAAATGGATAATGGCCGAAGCTTAACACGCCAACGCTCTTTAGA	650
251	HisLysCysGlyIleGlyArgSerTyRlysGlyArgSerSeLeuGlyLys	267
651	GGACATAAAGAGCCGCTGCCACAACACTTGAAAGCCATGGCCCTTCGG	700
267	uGluHisLysGlyIleGlySerMetGluSerMetGlyLeuPrcG	284
701	GCACACTGTACCGATCATTAAAGAGAACTAACACAGTGAATGGCA	750
284	ly...Metyl-ProValIleLysGlyLysGluLysGluLysGluLys	299
751	GAGACCTGTGAAGTAGGATCAAGAGATCTCUCGTGGACAGACT	800
300	GluAspLeuCysLysIleGlyAlaGluGua9SerLeuValLeuAspArgle	316
801	AGCAAGTAATGTCGCCAAAGCTAAAGCCTATGCCCTCAGAAATTCTTG	850
316	uAlaSerAsnValAlaLysArgLysSerSerMetProGlyLysLeuG	333
851	GGGACAAAGGGCCTGTCGGACAGGCCCTAGACAGTCCACCTGAGCAAGAG	900
333	IyAspLysCysLeuSerAspMetProTyAspSerAlaAsnTyRgluLys	349
901	GAGAAAGAAATGATGAGTGGTCACCTGATGCCAGTCAAGGAGAG	950
350	Glu...AspMetThrSerHisValMetAspGlnAlaIleAsnAsnAl	365
951	CATCAACTACCTGGGGGCCGAGTCCTGGCCCTGGTGGAGCAGGCC	1000
365	AlaLeuArgProValGlyAlaGluSerLeuArgProLeuValGinThrProp	382
1001	CGGGCGGGTCCGAGGGTGGTCGCCGTCATAGGCCGATGACAGTCAC	1050
382	LysProProSerAspGlyProToArgSerAsnHisSerAlaGlnAsp..	414
1098	CGCCGTGGAATCCGTCCTGCTCAGGCCAAGTGGTGGCCCTGC	1147

415	.AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValserG	431
1148	AGCGCCAGGGTCCGCCAGAACGCTGCCAAGACTCCAGCACCGAG	119
431	luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspHisGlu	447
1198	AGCAACAAAGGAGGACAGGCCAGGGCTATCATCTACCTGACCACCAT	124
448	SerAspAlaGluGluGlnArgSeGlyLeuIleTyriLeuThAsnHsII	464
1248	CGCCCGACGGCGAACGC...GTTGCGTCAAAGGAGGACGGCGCT	129
464	easnProHisAlaArgAsnGlyLeuAlaLeuIleLyglugIugInArgAla	481
1295	ACGACCTGTGCGGCCGCTCCAGAAACTCGCCAGAGGGCTCGCGCT	134
481	yrGluIvalLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal	497
1345	GTCAGGACCAAGCGGGAGGAGATGAGGGTAGACAGTGGAAACATGCGG	139
498	valSerThrSerGlyIgluGlnLeuLysValtrySlysGluHsCysAr	514
1395	GTTGCTCTTCTGTGATCACGTCATGTCACCATCACATG.....G	143
514	gvalLeuLeuAspHisValMetyltryTrileuIsmGlyCysHsG	531
1436	GCTGCCACGGCTTCGTTGATCCTTTGAGTGCACATGFGGGTACAC	148
531	1-lysylsGlyPheArgAspProHeGlucysAsnMetCysGlyTyrHis	547
1486	AGCAGGACCGGTACGAGTTCTGTCGCAATAAGCGANGGGCACCG	1533
548	SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisRr	564
1536	CRTCCAGATGACC	1548
564	gtryHisIleSer	568
seq_name: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/IA1996.DAT		
seq_documentation_block:		
D	D	AAR92021 standard; Protein; 470 AA.
C	X	AAR92021;
X	X	09-MAY-1996 (first entry)
X	E	Ikaros protein.
X	W	Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte; immunocomprised; immune system disorder; nervous system disease model.
X	W	Not specified.
X	H	Location/Qualifiers
T	1..2	Key
T	74	Misc-difference
T	163	/note= "unidentified amino acid"
T	184..186	Misc-difference
T	194	/note= "unidentified amino acids"
T	196	Misc-difference
T	207	/note= "unidentified amino acid"
T	236	Misc-difference
T	240	/note= "unidentified amino acid"

FT	Misc-difference	246	/note= "unidentified amino acid"
FT	Misc-difference	251..252	/note= "unidentified amino acid"
FT	Misc-difference	255	/note= "unidentified amino acids"
FT	Misc-difference	261	/note= "unidentified amino acid"
FT	Misc-difference	285	/note= "unidentified amino acid"
FT	Misc-difference	300..302	/note= "unidentified amino acids"
FT	Misc-difference	304	/note= "unidentified amino acids"
FT	Misc-difference	306	/note= "unidentified amino acid"
FT	Misc-difference	316	/note= "unidentified amino acid"
FT	Misc-difference	319..320	/note= "unidentified amino acids"
FT	Misc-difference	329	/note= "unidentified amino acid"
FT	Misc-difference	331	/note= "unidentified amino acid"
FT	Misc-difference	352	/note= "unidentified amino acid"
FT	Misc-difference	367..369	/note= "unidentified amino acids"
FT	Misc-difference	371..375	/note= "unidentified amino acids"
FT	Misc-difference	380	/note= "unidentified amino acid"
FT	Misc-difference	384..385	/note= "unidentified amino acids"
FT	Misc-difference	397	/note= "unidentified amino acid"
FT	Misc-difference	407	/note= "unidentified amino acid"
FT	Misc-difference	430..432	/note= "unidentified amino acids"
FT	Misc-difference	467	/note= "unidentified amino acid"
FT	Misc-difference	469	/note= "unidentified amino acid"
XX	PN	W09604372-A1.	
XX	PD	15-FEB-1996.	
XX	PF	28-JUL-1995;	95WO-US09345.
XX	PR	29-JUL-1994;	94US-0283300.
XX	(GEHO ) GEN HOSPITAL CORP.		
PA	Georgopoulos K;		
PI			
XX	DR	WPI; 1996-129389/13.	
XX			transgenic rodent harbouring Ikaros trans gene (pre-
PT			severely immuno-compromised and can be used as a
PT			effects of treatment for immune and nervous sys-
XX			Disclosure; Page 75-76; 102pp; English.
PS	XX		The sequence of an Ikaros Protein (AAIR2021) is
CC			specification. Ikaros protein is a master regu-
CC			hematopoietic differentiation and a major deter-
CC			differentiation. Isoforms of Ikaros (see AAR92)
CC			differential splicing of Ikaros gene transcripts,
CC			pref. mice, having a mutated Ikaros transgene,
CC			alters the DNA binding domain of the Ikaros pro-

CC models to determine the effects of treatments for immune or nervous  
CC system disorders.

XX Sequence 470 AA;

**alignment\_scores:**

Quality: 2207.50

Ratio: 5.098

Percent Similarity: 92.521

Percent Identity: 90.385

**alignment\_block:**

US-08-711-417c-165 x AAR92021 ..

Align seg 1/1 to: AAR92021 from: 1 to: 470

160 GCCAGTAATGTTAAAGTAGAGACTCAGACTGATGAAAGAACATGGCGTNGC 209  
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 3 AlaserAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19  
 210 CTGTGAATGATGGGAAAGAATGGGAACTGGGAACTGGGAGATTAGAAATGCTGATG 259  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 19 acysGluMetAsnGlyGluglucysAlaGluAspLysArgMetLeuAspA 36  
 260 CCTCGGGAGAAATGATGGTCCCACAGGACCAGGACCTGGCTCGCT 309  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 36 1aSerGlyGluLysMetAsnGlySerHsArgAspGlnGlySerAla 52  
 310 TGTCTGGGACTGGAGCACTTGCATTCGACTCTCTAAGGAAACATAAGTGTA 359  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 53 LeuSerGlyValGlyGlyLeuProAspGlyLysLeuLysCysAs 69  
 360 TATCTGTTGGATCATTTGCATCGGCCAANTGGCTCATGGTTCACAAA 409  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 69 PheLeuGlyIle\*\*CysLeuGlyIleLeuProAsnLeuLeuMetValHistysA 86  
 410 GAAGCCACACTGGAAAGGCCCTTCCAGTGAAATCAGTGGGGCCTCA 459  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 86 rSerHisthrGlyGluglucArgProHeGlnCysAsnGlnCysGlyAlaSer 102  
 460 TTCACCCAGGGCAACTCCGCAACTCAAGCTGCAATTCGGCAATCGGGGA 509  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 103 PhthrGlnLysGlyAsnLeuLeuArgHistyleuHsSerGlyG 119  
 510 GAACCCMPTCAAATGCCAACCTCTGCAACTACCCCTGCCGGGAGC 559  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 119 LysProHeGlnLysCysHisLeuCysAsnTyrAlaCysSargArgAspA 136  
 560 CCCCTACCTGGCACCTGAGGAGCAGCTCCGTTGGTAAACCTOCACATGT 609  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 136 LeuThrGlyHisLeuArgThrHisSerValGlyIysPheHisLysCys 152  
 660 AGGGCGTGGCCACAATGACTGAAAGCATGGCCGACACTGT 709  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 169 sGluArgCysHsAsnTyrLeuGluSerMetGlyLeuProGly\*\*\*\* 186  
 710 ACCCAGCTTAAAGAGRAACTAAAGCACAGTGAATGGCAGAACCTG 759  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 186 \*+proValLeuGlyGluThr\*\*\*His\*\*\*GluMetAlaGluAspLeu 202  
 760 TCCAAGATAGGTCAAGAGATCTCGTGGCACAGCTAGGAGTAA 809  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 203 cysLysIleGly\*\*GluArgSerLeuValLeuAspArgLeuAlaSerAs 219  
 810 TCTCGCCAAGGTAAGGCTCATGCTCTGAAATTCTPTGGGAGCAAGG 859  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 219 nvalAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys\* 236  
 860 .GCCTGTCCGACAGCCCTACGACAGTGGCACAGTACGAGAAAGCAA 909

236 \*\*LeuSerAsp\*\*\*ProTyrapSerAla\*\*\*TyrGluLyGlu\*\*\*\*\* 252

910 ATGATGAGTCCCCACCTGATGGACCAAGCCATCAACAGGCATCAACTA 959  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 253 MetMet\*\*SerHsValMetAsp\*\*\*AlaLeuAsnAlaLeuAsn 269

960 CCGGGGGCCGAGTCCCTGCGCCGCTGCTGAGGCCCCGGGGTT 1009  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 269 rIeugIyAlaGluSerLeuArgProLeuValGlnThrProProGly\*\*\*S 286

1010 CGAGGNGGTCCGGTCATCAGCCCCATGTCAGCTGAC...AGGGC 1056  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 286 ergLuValValProValLeuSerProMetTygInLeuHs\*\*\*\*\* 302

1057 TCGAGGGCACCCGGCGCTCCAAACCACTGCCAGAACGCGCGTGA 1106  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 303 Ser\*\*Gly\*\*\*ProArgSerAsnHsSeAlaGlnAsp\*\*\*AlaVal\*\* 319

1107 GTACCMCTGCTGCTGCTCAGGCCAAGTCTGGCCCTGGAGGCCGAGG 1156  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 319 \*\*\*LeuLeuLeuLeuSerValSallys\*\*\*Val\*\*\*SerGluArgGluA 336

1157 CTCCCCGAGAACAGCTGCAAGACTCACGGGAAACGGAGAACAAAC 1206  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 336 LaserProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn\*\*\* 352

1207 GAGGAGCGCCAGGGCTCTATCTACCTGACCAACCAATGCGCCGAGC 1256  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 353 GluGluGlnArgSerGlyLeuLeuThrIleThrHsle\*\*\*\*\*\* 369

1257 CGCG...CAACGGCGCCCTCCGAGAACTCGAGGAGCACGGCCATGACCMIC 1303  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 369 \*Ala\*\*\*\*\*LeuLysGluGlu\*\*\*ArgAlaTyr\*\*\*\*\*L 386

1304 TGCGCCGCCGCTCCGAGAACTCGAGGAGCACGGCCCTCGGCTGGTCAGCAC 1353  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 386 euArgAlaAlaSerGluAsnSerGlnAspAla\*\*\*ArgAlaValSerThr 402

1354 AGCGGGGAGGAGATGAACTGGCTGAACTGCAATGCTCTCTCTCT 1403  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 403 SerGlyGluLys\*\*\*LysValItyLysThrIleHsleMet\*\*\*\*\* 419

1404 CCTGGATCATGCTCATGTCACCAACCATG.....GGCTGCCACG 1444  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 419 eLeuAspHsValImetTythrIleHsleMet\*\*\*\*\*GlyCysHsG 436

1445 GCTTCGCTATCCTTTGATGTCACATGTCGGCTACACAGCCAGGAC 1494  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 436 lypheArgAspProHeGluCysAsnNetCysGlyTyrrHsleSerGluAsp 452

1495 CGPACGACTTCTCTGTCGGACATAGTCGGCTACACAGCCAGGAC 1544  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||:  
 453 ArgTygGluPheSerSerHsIleThrArgGlyGluHisArg\*\*\*His\* 469

1545 GAGC 1548  
 |||:  
 469 \*Ser 470

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:AAW72678

seq\_documentation.block:  
 ID AAW72678 standard; Protein: 470 AA.  
 XX AC  
 XX AAW72678;

XX DT 14-JAN-1999 (first entry)

XX DE Ikaros protein general formula.

XX KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;  
 KW differentiation marker; immune system; corpus striatum; AIDS;  
 KW Alzheimer's disease.

XX Homo sapiens. /note= "any amino acid"  
 XX Location/Qualifiers  
 FH Key  
 FT Misc-difference 1 /note= "any amino acid"  
 FT Misc-difference 2 /note= "any amino acid"  
 FT Misc-difference 74 /note= "any amino acid"  
 FT Misc-difference 163 /note= "any amino acid"  
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 FT Misc-difference 467 /note= "any amino acid"  
 FT Misc-difference 469 /note= "any amino acid"

XX US5824770-A.  
 PN XX 20-OCT-1998.  
 PD XX 05-JUN-1995; 95US-0465590.  
 PF XX 02-MAY-1994; 94US-0238212.  
 PR XX 14-SEP-1992; 92US-0946233.  
 PR XX 14-SEP-1993; 93US-0121438.  
 PR XX 05-JUN-1995; 95US-0465590.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX Claim 1; Column 127-130; 11pp; English.  
 PI Georgopoulos K;  
 XX WPT: 1998-582621/49.  
 DR XX  
 PT XX Ikaros poly-peptide(s) - useful for treating disorders of immune system or corpus striatum  
 PS XX  
 PS XX  
 CC The present invention describes a purified peptide having at least one sequence under the control of delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to delta A elements, NFkB elements, NFkB elements and/or Ikaros-binding oligonucleotides, delta A elements and/or Ikaros-binding oligonucleotides, delta A elements, NFkB elements, NFkB elements and/or Ikaros-binding oligonucleotides, competitively inhibit protein-protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. Alzheimer's disease. The present sequence represents an Ikaros protein general formula from the present invention.

XX Sequence 470 AA;  
 SQ XX

alignment\_scores:  
 Quality: 2207.50  
 Ratio: 5.098  
 Percent Similarity: 92.521  
 alignment\_block:  
 US-08-711-417C-165 x AAW72678 ..

Align seg 1/1 to: AAW72678 from: 1 to: 470

160 CCCAGTAATGTTAAAGTAGAGACTCGAGTGATGAGAAATGGCGGTGC 209  
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 3 AlaSerAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19

210 CCTGGAGAGAAAATGTAATGGCTCCACAGGGAACTCTGGCT 239  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 19 acySGLuMetLysGlyGluGluCysAlaGluAspLeuArgMetLeuAspA 36

260 CTCGGAGAGAAAATGTAATGGCTCCACAGGGAACTCTGGCT 309  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 36 IaSerGlyGluLysIetAsnGlySerHisArgaspGlyLysSerAla 52

310 TGTCTGGGAGTGGGCAATTGGGACTTCTAACCGAAACTAAAGTGTGA 359  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 53 LeuSerGlyAlaGlyGlyIleArgLeuProAsnClyLysLeuLysCYSAs 69

360 TATCTGTGGCATCTTGGATGCCAAATGGCTCATGGTCAACAAA 409  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 69 PileocysGlyIle\*\*\*CysIleGlyProAsnValleuMetValHisLysA 86

410 GAAGCCACACTGGAAACGCCACTTCCAGTCGAACTACTGGCCCTCA 459  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 86 rgsSerHistRglnGluLysArgPrDpheGlnCysAsnGlnCysGlyAaser 102

460 TTCACCCAGGGCAACCTGCTGGCACATCAAGCTGCTTCGGGA 509  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 103 PhePheGlnLysGlyAsnLysLeuLeuArgHisIleSerGlyGlyI 119

510 GAAGCCCTCAAAATGCCACCTCTGGCAACTACCCCTGCCGAGGACG 559  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 119 UlyProPheLysCysHisLeucysAsnTyralacysArgArgAspA 136

560 CCCCTACAGGCCACCTGGGACCCACTCCGGTGTAAACCTGAAATGT 609  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 136 IleLeuThrGlyHisIleArgThrHisSerValGlyLysPheHisLysCys 152

610 GGTATCTGGCGAACGTTAAAGGAAACTAACAGCGAACGCTCTTAGAGAACATAA 659  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 153 GlyTyrCysGlyArgSerTyrySglArg\*\*\*SerLeuGluLysIle 169

660 AGAGCGCTGCCACAACACTTGGGACCATGGGACACTGT 709  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 169 SGluArgGlyHisAsnTyLeuGluSerMetCysGlnArg\*\*\*SerGly 186

710 ACCAGCTATTAAGGAAACTAACAGCGAACGCTCTTAGAGAACATAA 759  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 186 \*provalleIeysGluGluThr\*\*\*Hist\*\*\*GluMetAlaGluAspLeu 202

760 TGCAGATAGGTCAAGAGATCTCGTGTGGAGACTAACGACTAA 809  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 203 CysLysIleGly\*\*\*GluArgSerLeuValLeuAspArgLeuAseras 219

810 TGTGCCAAACCTAACGCTCTATGCCATCAAATTCTGGGACAAGG 859  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 219 nvalAlaLysArgLySerSerMetProGlnLysPheLeuGlyAspLys\* 236

860 GCTGTCTGGACAGCCCTAACGACAGTACGAGAAAGGAGAACGAA 909  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 236 \*LeuSerAsp\*\*\*ProtYrasSerAla\*\*\*TyrGluLysGlu\*\*\*\*\* 252

910 ATGATGAAGTCCACGGTGTGGACCAAGCCATCAACAAAGCCATCAACTA 959  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

253 MetMet\*\*\*SerHisValMetAsp\*\*\*AlaLeuAsnAlaLeuAsnT 269  
 960 CCTGGGGGCCGAGTCCTGGCCGGCTGGTGAAGCCCGGGGGTT 1009  
 269 rleugIyAlaGluSerLeuArgProLeuValGlnThrProProGly\*\*S 286  
 1010 CCGAGGTGTCGGGTATCACCCGATGTTACAGCTGAC..AGGCAC 1056  
 266 ercluIvalProValIleSerProMetYrgIleUehLs\*\*\*\*\* 302

1057 TCGGAGGGCACCCGGCTCCAACCACTCGGCCAGGACAGCGCGTGGGA 1106  
 303 Ser\*\*\*Gly\*\*ProArgSerAsnHisSerAlaGlnAsp\*\*\*AlaVal\*\* 319

1107 GTTACCCGCTGCTGCTTCAGGCCAGTGTGCCTCGAGGCCGAGG 1156  
 319 \*\*\*LeuIleLeuSerlysAlaLys\*\*\*Val\*\*\*SerGluArgGluA 336

1157 CGTCCCCAGAACACCTGCCAAGACTCACGGACACGGAGAACAAAC 1206  
 336 IaSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn\*\* 352

1207 GAGGAGGAGCAGGGCTTATCPACCTGACCACATCGCCGACCG 1256  
 353 GluGluGlnArgSerGlyLeuIleIlyLeuThrAsnHisIle\*\*\*\*\* 369

1257 CGCG...CAAGCGGTGTCGCTCAAGGAGAACGACCGGCCTACGACCTCGC 1303  
 369 \*Ala\*\*\*\*\*LeuIleLeuSerlysLeuIleLeuIleLeuIleLeuIle 386

1304 TGCGGCCGCGCTCCGAGAACACTCGAGAACGGCTCCGCTGGTCAGCAC 1353  
 386 euargAlaIaSerGluAsnSerGlnAspAla\*\*\*ArgAlaValSerhr 402

1354 AGCGGGAGGAGATGAAGGTGACAGTGGAAACTGGGGGCTGCTCT 1403  
 403 SerGlyGluGln\*\*\*LysValty-LysCysGluHisCysArgValLeuPh 419

1404 CCTGATCATCGCTCATGTCACCACTG.....GGCTGCCAG 1444  
 419 eLeuAspHisValMetTyThrIleHistMet\*\*\*\*\*GlyCysHISG 436

1445 GCTTCGTTGATCCCTTGTGACTGAACTCATGCGGCTACACAGCCAGGAC 1494  
 436 LysPheArgAspProDheGluCysAsnMeccyGlyTyHisSerGlnAsp 452

1495 CGGTACGAASTTCGTCGACATAACGGGAGGGAGCACGCTTCCACAT 1544  
 453 ArgTyrgIapheserSerSerIleIleThrArgGlyGluHisArg\*\*\*His\*\* 469

1545 GAGC 1548  
 469 \*Ser 470

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT :AAW70970  
 seq\_documentation\_block:  
 ID AAW70970 standard: Protein; 470 AA.  
 XX  
 AC AAW70970;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Ikaros isoform 1 consensus.  
 XX  
 KW Ikaros; MIK-1; transcription factor; mouse; human;  
 KW lymphocyte; cell differentiation; T cell; cancer;  
 KW immunodeficiency; Alzheimer's disease; therapy; diagnosis.  
 XX  
 OS Mus sp.  
 XX  
 FH Key  
 FT Misc-difference Location/Qualifiers

FT Misc-difference 2 /note= "variable"  
 FT Misc-difference 74 /note= "variable"  
 FT Label= Gly, Ala, Val, Ile, Leu, Ser, Thr  
 FT Misc-difference 89 /note= "the codon for Thr-89 may be made  
     degenerate to provide a stop codon in  
     recombinant genes of a degenerate library"  
 FT Misc-difference 145 /note= "the codon for Ser-145 may be made  
     degenerate to provide a stop codon in  
     recombinant genes of a degenerate library"  
 FT Misc-difference 163 /note= "variable"  
 FT Misc-difference 184 /note= "variable"  
 FT Label= Gly, Ala, Val, Ile, Leu, Ser, Thr  
 FT Misc-difference 185 /note= "residue 184 may also not be present"  
 FT Misc-difference 186 /note= "variable"  
 FT Misc-difference 187 /note= "the codon for Pro-187 may be made  
     degenerate to provide a stop codon in  
     recombinant genes of a degenerate library"  
 FT Misc-difference 194 /note= "variable"  
 FT Misc-difference 196 /note= "variable"  
 FT Misc-difference 207 /note= "variable"  
 FT Misc-difference 232 /note= "variable"  
 FT Misc-difference 236 /note= "variable"  
 FT Misc-difference 240 /note= "variable"  
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XX CA2194256-A.  
 PN 05-MAR-1998.  
 XX 97CA-2194256.  
 PF 02-JAN-1997;  
 XX 96US-0711417.  
 PR 05-SEP-1996;  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PI Georgopoulos K;  
 XX WPI; 1998-370292/33.  
 DR Disclosure; Page 59-60; 158PP; English.  
 XX This is an example of a polypeptides derived from a  
 CC degenerate library of polypeptides based on the amino acid  
 CC sequences of human and murine Ikarsis isoform 1 proteins hik-1 (see  
 CC AAW70964) and mik-1 (see AAW70965). A combinatorial library is  
 CC produced using a degenerate library of genes which each include  
 CC at least a portion of potential Ikarsis sequences. It can be  
 CC generated by combinatorial mutagenesis at the nucleic acid level.  
 CC Native Ikarsis is active in the early stages of lymphocyte  
 CC differentiation. Different isoforms arise from differential  
 CC splicing of Ikarsis gene transcripts. They are expressed primarily  
 CC in T cells in the adult and may play a role as a genetic switch  
 CC regulating entry into the T cell lineage. The invention provides  
 CC Ikarsis nucleic acids (see AAV42885-11 and AAV42840), polypeptides (see  
 CC AAW70963-71), vectors and host cells. These can be used to treat T

and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or cancer), to control expression of heterologous genes placed under control of an IkBα responsive element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplification or differentiation, especially in hematopoietic cells. Some IkBα isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences.

DE Murine Ikaros protein mIK-3.  
 XX Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;  
 KW immunocomprised; immune system disorder; nervous system disorder;  
 KW animal model; mIK-3.  
 XX OS Mus musculus.  
 PN WO9604372-A1.  
 XX PD 15-FEB-1996.  
 XX PF 28-JUL-1995; 95WO-US09345.  
 XX PR 29-JUL-1994; 94US-0283300.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PI Georgopoulos K;  
 XX DR WPI; 1996-129389/13.  
 DR N-PSDB; AAT16061.  
 XX PT Transgenic rodent having Ikaros trans-gene (pref. mutated) - is  
 PT severely immuno-compromised and can be used as model to determine  
 PT effects of treatment for immune and nervous system disorders  
 XX Disclosure; Page 63-64; 102pp; English.  
 CC The sequence of 48 kDa mouse Ikaros protein mIK-3 (AAR92016) was  
 CC deduced from mouse Ikaros cDNA (AAT16061) isolated from a mature  
 CC T-cell line E15 library. Ikaros protein is a master regulator of  
 CC hematopoietic differentiation and a major determinant in lymphocyte  
 CC differentiation. Other isoforms of Ikaros (see AAR92014 and  
 CC AAR92017-19) arise from differential splicing of Ikaros gene  
 CC transcripts. Transgenic animals, esp. mice, having a mutated Ikaros  
 CC protein, are used as models to determine the DNA binding domain of the  
 CC treatments for immune or nervous system disorders.  
 XX SQ Sequence 432 AA;

alignment\_scores:  
 Quality: 1963.00 Length: 521  
 Ratio: 4.776 Gaps: 6  
 Percent Similarity: 78.887 Percent Identity: 74.280

alignment\_block:  
 US-08-711-417C-165 x AAR92016 ..

Align seg 1/1 to: AAR92016 from: 1 to: 432

1 ATGGATGCTGAGGAGGTCAAGACATCTCTTCATCAGGAAGGAAG 50  
 1 MetAspValAspSerGluGlyLysAspMetSerGlnValSerGlyLysGlue 17  
 51 CCGAGGACCTCCACACCCTGGAGCACQCAAAGCTCAAGGTGAC 150  
 17 rProProValSerAspThrProAspGluGlyLysAspGluProMetProValP 34  
 101 CGCAGGACCTCCACACCCTGGAGCACQCAAAGCTCAAGGTGAC 150  
 34 roGluAspLeuSerThrThrSerGlyAlaGlnAsnSerLysSerAsp 50  
 151 AGAGCTGCGGCCGAGTAATGTTAAAGTAGACTCAGAGTGTAGAGAGAA 200  
 51 ArgGlyMetalAspSerAsnValIysValGluThrGlnSerAspGluAs 67  
 201 CGGGCGCGCCCTGAAATGAAAGGAAAGATGTCGGAGATTACGAA 250  
 67 nGlyArgAlaCysGluMetAsnGlyLysGluCysAlaGluAspLysArgM 84

251 TGCTTGATGGCTCGGGAGGAAAATGAAATGGCTCCCACAGGGACCAAGGC 300  
 84 etLeuAspAlaSerGlyLysMetAsnGlySerHisArgAspGluGly 100  
 301 AGCTGGCTTTGTCGGAGTTGGAGCATTCGACTTCCATACGGAAACT 350  
 101 SerSerAlaLeuSerGlyValGlyLysLeuArgLeuProAsnGlyLysLe 117  
 351 AAAGTGTGATACTCTGGATCATTTGATCTGGCCCCATGGTCATGG 400  
 117 uLysCysAspPleGlyLysLeuValCysteGlyProAsnValLeuMetV 134  
 401 TTACACAAAGAACGGCCACACTGGAGAACGCCCTTCAGTCAAATCAGRC 450  
 134 alaHisLysArgSerGlyLysTrpGluArgProPheGlyLysAsnGinSe 150  
 451 GGGCCTCATTCACCCAGAAGGGCACCTGCTCGGCACATCAAGCTGCA 500  
 151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisLysLeuHi 167  
 501 TTCCGGGAAAGGCCCTAAATGCCACCTCTGAACTACAGCTGCCGCC 550  
 167 sserGlyGluLysProPheLysCysThrHisLeuCysAsnTrpAlaCysArgA 184  
 551 GGAGGACGCCCTCACTGGCCACCTGTGAGCAGCAGCTCCGTTGGTAAACCT 600  
 184 tgaTgAspAlaLeuThrGlyHisLeuA9ThrHisSer..... 196  
 601 CACAAATGTTGGATATTGGCCGAAAGCTATAAACGGAAACGCTTTAGA 650  
 196 ..... 196  
 651 GGAACATAAGAGGCGCTGCCACAACTACTGGAAAGCATGGCTTCGG 700  
 196 ..... 196  
 701 GCACACTGACCCAGTCATTAAAGAAACTAAAGCAGTGAATGGCA 750  
 196 ..... 196  
 751 GAAGACCTGTGCAAGATAGGATCAGAGAGTCCTCGTGTGGACAGACT 800  
 196 ..... 196  
 801 AGCAAGTAATGTCGCCAAAGCTAAAGACTCTAGCCTCAAGAAATTCTCTG 850  
 197 ..... 197  
 851 GGGACAAGGGCCTGTCGACAGCAGCTGCACTGTCAGTAGAGAG 900  
 197 LysAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 213  
 901 GAGACGAAATGATGAAAGTCCACGTATGGCCAAGGCAATACAACGC 950  
 214 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnA 229  
 951 CATCAACTACCTGGGGCGAGTCCTCTGCCGCTGCTGAGCAGC 1000  
 229 aIleAsnTrpLeuGlyAgluSerLeuArgProLeuValGlnThrProP 246  
 1001 CGGGGGTTCGGAGTGGTCCCCTGTCAGCCGATGATACAGCTGCAC 1050  
 246 roGlySerSerGluValProValIleSerSerMetYrgInLeuHi 262  
 1051 AGG...CGGCTGGAGGCGGCCGAGCCACACTGCGCCAGGACAG 1097  
 263 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAspP.. 278  
 1098 CGCCGTGGAGTACCTGCTGCTCTCCAGGCAAGTGGTGCCTCTCG 1147  
 279 .AlaValAspAsnLeuLeuSerIysAlaLysSerValSerSerG 295  
 1148 AGCGCGAGGCGTCCCGAGCAACAGCTGCCAAAGACTCCAGGACACCGAG 1197

||||| 1uArgGluIaSerProSerIaSerSerCysGlnAspSerThrAspThrGlu 311  
 295 1uArgGluIaSerProSerIaSerSerCysGlnAspSerThrAspThrGlu 311  
 1198 AGCAACAACGAGGAGCGAGCCGCTTCTATCTGACCACCAT 1247  
 312 SerAsnAlaGluGluGlnArgSerGlyLeuThrAsnHistI 328  
 1248 CGCCGCGAGGGCAACGG...GTGTCGTCGAAGGAGACCCGGCT 1294  
 328 easnProHisIaArgAsnGlyLeuAlaLeuIysGluGluGlnArgAlaI 345  
 1295 AGGACCGCTGCGCGCCCTCGAGGAACTCGCAGGACCGCTCCGCG 1344  
 345 YrIuvalLeuIaLearGaiAaLaserGuaIaSerGlnAspAlaPheArgVal 361  
 1345 GTCAGCACCGGGGAGGAGATGAGGTGTAACAATGCCAACATGCCG 1394  
 362 ValserIaSerGlyIuGlnLeuIysValtrylScyGluHisCysAr 378  
 1395 GGTTGCTCTCGGATCACGTAATGTAACCATCACATG...G 1435  
 378 gIaIleuPhelIeuaPhisValMetYrrIleHsMetGlyCysHisG 395  
 1436 GCTGCCAACGGCTTCCGGTATCCTTGTAGTCACATGTCGGCTACAC 1485  
 395 1ycyHisIgLyPheIaArgAspPpropeGluCysAsnMetCysGlyTyrHis 411  
 1486 AGCCAGAACGGTACCGAGGTTCCTCGTCACATAACCGGAGGACACCG 1535  
 412 SerGlnAspArgTyrGluPheSerSerHistIeIArgGlyGluHisAr 428  
 1536 CTCACCATGAC 1548  
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 ID AAW72673 standard; Protein: 432 AA.  
 XX AAW72673;  
 XX DT 14-JAN-1999 (first entry)  
 XX DE Mouse Ikarus mIk-3.  
 XX KW CD3-delta gene; Ikarus gene; T cell; progenitor stem cell; leukaemia;  
 KW differentiation marker; immune system; corpus striatum; AIDS;  
 KW Alzheimer's disease.  
 XX OS Mus sp.  
 XX US5824770-A.  
 XX PD 20-OCT-1998.  
 XX PF 05-JUN-1995; 95US-0465590.  
 XX (GEHO ) GEN HOSPITAL CORP  
 XX PR 02-MAY-1994; 94US-0238212.  
 PR 14-SEP-1992; 92US-0946333.  
 PR 14-SEP-1993; 93US-0121438.  
 PR 05-JUN-1995; 95US-0465590.  
 XX DR WPI: 1998-582621/49.  
 N-PSDB; AA766970.  
 XX PT Ikaros poly:peptide(s) - useful for treating disorders of immune  
 system or corpus striatum  
 PT alHisLysArgSerHistIgLyGluIaGProHeGlnCysAsnGinSer 150  
 XX

PS Claim 1; Column 57-62; 111pp; English.  
 XX  
 CC The present invention describes a purified peptide having at least one  
 CC of the following properties: (a) it stimulates transcription of a DNA  
 CC sequence under the control of a delta A element, an NFkB element or an  
 CC Ikarus binding oligonucleotide consensus sequence; (b) it binds to any of  
 CC a delta A element, an NFkB element or an Ikarus binding oligonucleotide  
 CC consensus sequence; (c) it competitively inhibits the binding of a  
 CC naturally occurring Ikarus isoform to any of a delta A element, an NFkB  
 CC element or an Ikarus binding oligonucleotide consensus sequence; (d) it  
 CC competitively inhibits Ikarus binding to Ikarus responsive elements; or  
 CC (e) it inhibits protein-protein interactions of transcriptional complexes  
 CC formed with naturally occurring Ikarus isoforms. The proteins, provided  
 CC that they stimulate gene transcription under the control of delta A  
 CC elements, NFkB elements and/or Ikarus-binding oligonucleotides, bind to  
 CC delta A elements, NFkB elements and/or Ikarus isoforms to  
 CC competitively inhibit binding of naturally occurring Ikarus isoforms to  
 CC delta A elements, NFkB elements and/or Ikarus-binding oligonucleotides,  
 CC competitively inhibit Ikarus binding to Ikarus-responsive elements and/or  
 CC inhibit protein-protein interactions of transcriptional complexes with  
 CC naturally occurring Ikarus isoforms, can be used to treat immune system  
 CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.  
 CC Alzheimer's disease. The present sequence represents a specifically  
 CC claimed mouse Ikarus protein.  
 XX Sequence 432 AA;  
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 US-08-711-417C-165 x AAW72673 ...  
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 Percent Similarity: 78.887 Length: 521  
 Ratio: 4.776 Gaps: 6  
 Percent Identity: 74.280  
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 51 CCCCCCTGTAAGCGATACTCCAGATGAGGCGATGACCCATGCCGATTC 100  
 17 rProProValSerAspIhrProAspGluIuGlyAspGluProMetProValP 34  
 101 CCGAGGACTCTCCACACTCGGGAGGACAGCAAAGCTCCAAAGACTGAC 150  
 34 roGluAspIleusSerThrSerGlyIaIglnAsnSerIysSeAsp 50  
 151 AGACTCGTGGCCAGTAGTAAAGTACAGACTCAGGTGAGGAAGAAA 200  
 51 ArgClyMetAlaSerAspValIlyValSerGluIuAspGluIuAs 67  
 201 TGGCGTGCCTGTTGAATGGGAAGAAGTGCGGAGGATTAGCA 250  
 67 nGlyArgAlaCysGluMetAsnGlyIuGlyAspIleuArg 84  
 251 TGCTTGATCCCTCGGGAGAAATGATGTTGAGGATTCGACTTCCTAACGGAAACT 300  
 84 etIleuAspIlaSerGlyIuGlyIuSmetsAsnGlySerHsargAspGlnGly 100  
 301 AGCTCGGGCTTGTGGGAGTTGGAGGATTCGACTTCCTAACGGAAACT 350  
 101 SerSerAlaLeuSerGlyIuGlyIuLeuProAspGlyLysIle 117  
 351 AAAGCTGTGATATCTGTTGGATCATTTGCATCGGGCCAAATGNGCTCATGG 400  
 117 uLysCysAspIleCysGlyIuIleValCysIleGlyProAsnValLeuMetV 134  
 401 TTCAAAAGGAAGCCACACTGGAGAACGCCCTCCAGTCATCAGTC 450  
 134 alHisLysArgSerHistIgLyGluIaGProHeGlnCysAsnGinSer 150  
 XX



